DNA sequences in Enchytraeidae taxonomy, a progress report

SCHMELZ Rüdiger M.1,2, COLLADO Rut1, PORCO David3, VIERA Joaquín4, RÖMBKE Jörg1

1ECT Oekotoxikologie GmbH, Flörsheim, Germany
2University of A Coruña, Science Faculty, Department of Animal Biology, Plant Biology and Ecology, Spain
3Université de Rouen, Laboratoire ECODIV, Mont Saint Aignan, France
4AllGenetics, A Coruña, Campus de Elviña, Spain
e-mail: rmschmelz@gmail.com, j-roembke@ect.de, rutco@udc.de, david.porco.gm@gmail.com, joaquin@allgenetics.eu

Taxonomy of enchytraeids is usually lagging behind the current trends, but the last five years have seen an increasing integration of DNA sequences into the taxonomic and systematic work with this group. Reviewing the literature and reporting work in progress of our own initiatives, we give an account of the state of the art and we critically assess the potential of DNA sequences in Enchytraeidae taxonomy using a few case studies as examples. DNA sequences provide an independent second dataset that allows to falsify or to confirm hypotheses based on morphological work. Molecular phylogenies help to interpret character changes and evolution within the group, which means nothing less than to understand the extant patterns of diversity. At the species level DNA sequences have unveiled cryptic diversity but also the contrary, synonymies of species. Large-scale barcoding of common terrestrial species may allow automated sequence-based identification of selected sites in the near future. Together with sound morphological work, DNA-based taxonomy opens a new era of Natural History.

Oral presentation at 6th International Oligochaete Taxonomy Meeting, Palmeira do Faro, Portugal, April 22 - 25, 2013.